

AMENDMENTS

AMENDMENTS TO THE CLAIMS

Please amend the claims as set out in the listing below:

1. (Previously presented) A method of predicting the likelihood of long-term survival without recurrence of breast cancer for a patient having estrogen receptor (ER)-positive breast cancer, the method comprising:

(a) assaying an expression level of an RNA transcript or its expression product in a biological sample comprising a breast cancer cell obtained from the patient, wherein the RNA transcript is a MYBL2 transcript;

(b) determining a normalized expression level of the MYBL2 transcript or its expression product, wherein the normalized expression level of the MYBL2 transcript or its expression product positively correlates with an increased likelihood of breast cancer recurrence in the patient; and

(c) providing information regarding the likelihood of breast cancer recurrence for the patient, wherein the information comprises the normalized expression level of the MYBL2 transcript or its expression product.

2. – 5. (Canceled)

6. (Original) The method of claim 1 wherein breast cancer is invasive breast carcinoma.

7. (Canceled)

8. (Previously presented) The method of claim 1 wherein the biological sample is a fixed, wax-embedded breast cancer tissue specimen .

9. (Previously presented) The method of claim 1 wherein the biological sample is isolated from core biopsy tissue or fine needle aspirated cells.

10-24. (Canceled)

25. **(Currently amended)** A method of preparing a personalized genomics profile for a patient with estrogen receptor (ER)-positive breast cancer, comprising the steps of:

(a) assaying an expression level of an RNA transcript or its expression product in a biological sample comprising a breast cancer cell obtained from the patient, wherein the RNA transcript is a MYBL2 transcript;

(b) determining a normalized expression level of the MYBL2 transcript or its expression product, wherein the normalized expression level of the MYBL2 transcript or its expression product positively correlates with an increased likelihood of breast cancer recurrence in the patient; and

(c) creating a report summarizing data obtained from the normalized expression level and containing an estimate of likelihood of long-term survival without breast cancer ~~recurrence~~ recurrence in said patient.

26. (Canceled)

27. (Previously presented) The method of claim 25, wherein the biological sample is a fixed, paraffin-embedded biopsy sample.

28. (Previously presented) The method of claim 25 wherein the RNA transcript is fragmented.

29. (Canceled)

30. (Previously presented) The method of claim 25 further comprising identifying a treatment option for the patient based on the normalized expression level.

31-35. (Canceled)

36. (Previously presented) The method of claim 1 wherein the expression level of the MYLB2 transcript, or its expression product, is normalized against a reference set comprising RNA transcripts of two or more housekeeping genes, or their expression products.

37. (Previously presented) The method of claim 36 wherein the two or more housekeeping genes are selected from the group consisting of glyceraldehyde-3-phosphate dehydrogenase (GAPDH), Cyp1, albumin, actins, tubulins, cyclophilin, hypoxanthine phosphoribosyltransferase (HRPT), L32, 28S, and 18S.

38. - 55. (Canceled)

56. (Previously presented) The method of claim 1, further comprising

(a) assaying an expression level of at least one RNA transcript or its expression product in a biological sample comprising at least one breast cancer cell obtained from the patient, wherein the at least one RNA transcript is the transcript of a gene selected from the group consisting of: GRB7, CTSL, CD68, Chk1, AIB1, CCNB1, MCM2, FBXO5, STK15, SURV, EGFR, HIF1 α , and TS;

(b) determining a normalized expression level of the RNA transcript or its expression product, wherein the normalized expression level of the RNA transcript or its expression product positively correlates with an increased likelihood of breast cancer recurrence; and

(c) providing information comprising the likelihood of long-term survival without breast cancer recurrence for the patient, wherein the information comprises the normalized expression level of the RNA transcript or its expression product.

57. (Previously presented) The method of claim 1, further comprising

(a) assaying an expression level of at least one RNA transcript or its expression product in a biological sample comprising at least one breast cancer cell obtained from the patient, wherein the at least one RNA transcript is the transcript of a gene selected from the group consisting of: TP53BP2, Bc12, KRT14, EstR1, IGFBP2, BAG1, CEGP1, KLK10, β -Catenin, γ -Catenin, DR5, P13KCA2, RAD51C, GSTM1, FHIT, RIZ1, BBC3, TBP, p27, IRS1, IGF1R, GATA3, ZNF217, CD9, pS2, ErbB3, TOP2B, MDM2, IGF1, and KRT19;

(b) determining a normalized expression level of the at least one RNA transcript or its expression product, wherein the normalized expression level of the at least one RNA transcript or its expression product negatively correlates with an increased likelihood of breast cancer recurrence.

58. (Previously presented) The method of claim 1 further comprising determining the normalized expression level of a PR RNA transcript or its expression product, wherein the the

normalized expression level of PR negatively correlates with an increased likelihood of breast cancer recurrence.

59. (Previously presented) The method of claim 1 further comprising determining a normalized expression level of a Her2 RNA transcript or its expression product, wherein the normalized expression level of Her2 negatively correlates with an increased likelihood of long-term survival without breast cancer recurrence .

60. (Previously presented) The method of claim 1 further comprising in step (a) determining the expression level of the PR RNA transcript or its expression product in a breast cancer tissue sample obtained from said patient, normalized against the expression levels of all RNA transcripts or their expression products in said breast cancer tissue sample, or of a reference set of RNA transcripts or their products.

61. (Previously presented) The method of claim 1 or claim 60 further comprising in step (a) determining the expression level of the Her2 RNA transcript or its expression product in a breast cancer tissue sample obtained from said patient, normalized against the expression levels of all RNA transcripts or their expression products in said breast cancer tissue sample, or of a reference set of RNA transcripts or their products.

62. (Previously presented) The method of claim 25 further comprising in step (b) determining the expression level of PR, wherein the expression level is normalized against a control gene or genes and optionally is compared to the amount found in a breast cancer reference tissue set.

63. (Previously presented) The method of claim 25 or claim 62 further comprising in step (b) determining the expression level of Her2 wherein the expression level is normalized against a control gene or genes and optionally is compared to the amount found in a breast cancer reference tissue set.

64.– 66. (Canceled)

67. (Previously presented) The method of claim 1, wherein the information is provided in the form of a report.

68. (Previously presented) The method of claim 56, wherein the information is provided in the form of a report.